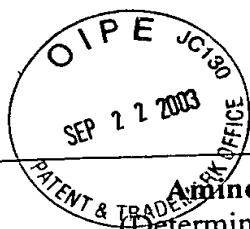


## **EXHIBIT 1**



**Amino Acid Sequence Homology Between Heat Shock Proteins**  
(Determined Using BLAST 2.2.3 (<http://www.ncbi.nlm.gov/blast/bl2seq>))

		% Identical Amino Acids	% Similar Amino Acids	Comments
GroEL ( <i>E. coli</i> )	HSP60 (human)	50	71	
Cpn10 (human)	GroES ( <i>E. coli</i> )	38	60	
Cpn10 (human)	GroEL ( <i>E. coli</i> )			No Significant Similarity Found
Cpn10 (human)	Hsp70 (human)			No Significant Similarity Found
Cpn10 (human)	Hsp90 (human)			No Significant Similarity Found
Cpn10 (human)	Gp96 precursor (human)			No Significant Similarity Found
Hsp90 (human)	Gp96 precursor (human)	47	65	
Hsp90 (human)	GroEL ( <i>E. coli</i> )			No Significant Similarity Found
Hsp90 (human)	HSP60 (human)			No Significant Similarity Found
Hsp90 (human)	Hsp70 (human)			No Significant Similarity Found
Cpn10 (human)	Hsp60 (human)			No Significant Similarity Found
Hsp60 (human)	GroES ( <i>E. coli</i> )			No Significant Similarity Found
Hsp60 (human)	Hsp70 (human)			No Significant Similarity Found
Hsp60 (human)	Gp96 precursor (human)			No Significant Similarity Found
Hsp70 (human)	GroES ( <i>E. coli</i> )			No Significant Similarity Found
Hsp70 (human)	Gp96 precursor (human)	24	41	

**RECEIVED**

OCT 02 2003

**TECH CENTER 1600/2900**



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

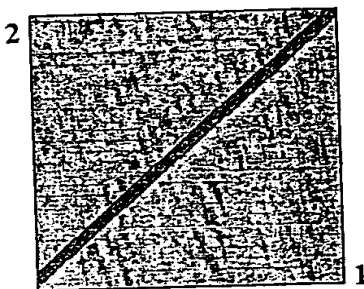
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix BLOSUM62 gap open: 11 gap extension: 1x\_dropoff: 50 expect: 10.00 wordsize: 3 Filter ☐ None

Sequence 1 gi 1790586 GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein [Escherichia coli.K12] Length 548 (1..548)

Sequence 2 gi 306890 chaperonin (HSP60) Length 573 (1..573)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 548 bits (1413), Expect = e-155  
Identities = 278/548 (50%), Positives = 396/548 (71%), Gaps = 4/548 (0%)

```

Query: 3   AKDVKFGNDARVKMLRGVNLADAVKVTLGPKGRNVVLDKSFSGAPTITKDGVSVAREIEL 62
          AKDVKFG DAR ML+GV++LADAV VT+GPKGR V++++ +G+P +TKDGV+VA+ I+L
Sbjct: 27  AKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIIEQGWGSPKVTKDGVTVAKSIDL 86

Query: 63  EDKFENMGAQMVKEVASKANDAAGDGTATVLAQAIITEGLKAVAAGMNPMDLKRGRIDK 122
          +DK++N+GA++V++VA+ N+ AGDGTATVLA++I EG + ++ G NP++++RG+
Sbjct: 87  KDKYKNIGAKLVQDVANNTNEEAGDGTATVLAQAIITEGLKAVAAGMNPMDLKRGRIDK 146

Query: 123  AVTAAVEELKALSVPSCSKAIAQVGTISANSDETGVKLI AEAMDKVGKEGVITVEDGTG 182
          AV A + ELK S P + + IAQV TISAN D+ +G +I++AM KVG++GVITV+DG
Sbjct: 147  AVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKT 206

Query: 183  LQDEL DVVEGMQFDRGYLSPYFINKPETGAVELES PFILLADKKISNIREMLPVLEAVAK 242
          L DEL+++EGM+FDRGY+SPYFIN + E + ++LL++KKIS+I+ ++P LE
Sbjct: 207  LNDELEIIEGMKFDRGYISPYFINTSKGQKCEFDAYVLLSEKKISSIQSIVPALEIANA 266

Query: 243  AGKPLLI AEDVEGEALATLVNTMRGIVKVA AVKAPGFGDRRKAMLQDIATLTGGTVIS 302
          KPL+IIAEDV+GEAL+TLV+N ++ ++V AVKAPGFGD RK L+D+A TGG V
Sbjct: 267  HRKPLVIIAEDVDGEALSTLVNRLKVLQVAVKAPGFGDNRKNQLKDMAIATGGAVFG 326

Query: 303  EE-IGMELEKATLEDLGQAKRVVINKDTTIIIDGVGEEAAIQGRVAQIRQQIEEATSDYD 361
          EE + + LE DLG+ V++ KD ++ G++A I+ R+ +I +Q++ TS+Y+
Sbjct: 327  EEGLTLNLEDVQPHDLGKVGIVTKDDAMLLKKGKDKAQIEKRIQEIEQLDVTTSEYE 386
  
```

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?>

7/29/2002

Query: 362 REKLQERVAKLGGVAVIKVGAATEVEMKEKKARVEDALHATRAAVEEGVVAGGGVALIR 421  
+EKL ER+AKL+ GVAV+KVG ++VE+ EKK RV DAL+ATRAAVEEG+V GGG AL+R  
Sbjct: 387 KEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDRVTDALNATRAAVEEGIVLGGGCALLR 446

Query: 422 VASKLADLRGQNEQNVGIKVALRAMEAPLRQIVLNCGEEPSVVANTVKGGDGNYGYNAA 481  
L L NEDQ +GI++ R ++ P I N G E S++ + GY+A  
Sbjct: 447 CIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIKVNAGVEGSLIVEKIMQSSSEVGVDAM 506

Query: 482 TEEYGNMIDMGILDPTKVTRSAALQYAASVAGLMITTECMVTDLPKNDA-ADLGAAGGMGG 540  
++ NM++ GI+DPTKV R+AL AA VA L+ T E +VT++PK + +GA GGMG  
Sbjct: 507 AGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGAMGGMG- 565

Query: 541 MGGMGGM 548  
GGMGG M  
Sbjct: 566 -GGMGGGM 572

CPU time: 0.13 user secs. 0.03 sys. secs 0.16 total secs.

Lambda	K	H
0.313	0.132	0.351

## Gapped

Lambda	K	H
0.267	0.0410	0.140

## Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 3820

Number of Sequences: 0

Number of extensions: 355

Number of successful extensions: 4

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 548

length of database: 327,972,341

effective HSP length: 128

effective length of query: 420

effective length of database: 251,365,749

effective search space: 105573614580

effective search space used: 105573614580

T: 9

A: 40

X1: 16 ( 7.2 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 42 (21.9 bits)

S2: 75 (33.5 bits)



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

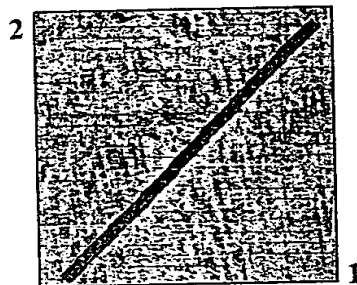
Structure

## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix BLOSUM62 gap open: 11 gap extension: 1  
 x\_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☐ Align

Sequence gi heat shock 10kD protein 1 (chaperonin 10) [Homo sapiens] Length 102 (1..102)  
 1 4504523

Sequence gi GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP, Length 97 (1..97)  
 2 1790585 suppressing its ATPase activity [Escherichia coli K12]



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 64.3 bits (155), Expect = 8e-11  
 Identities = 34/88 (38%), Positives = 54/88 (60%), Gaps = 1/88 (1%)

Query: 11 PLFDRVLVERSAETVTKGGIMLPEKSQGVQLQATVVAVGSGSKGKGGEIQPVSVKVGDK 70  
 PL DRV+V+R ET + GGI+L + K + V+AVG+G + GE++P+ VKVGD  
 Sbjct: 5 PLHDRVIVKRKEVETKSAGGIVLTGSAARKSTRGEVLAVGNRILENGEVKPLDVKVGDI 64

Query: 71 VLLPE-YGGTKVVLDDKDYFLFRDGDIL 97  
 V+ + YG +D+++ + + DIL  
 Sbjct: 65 VIFNDGYGVKSEKIDNEEVLMSESIL 92

CPU time: 0.02 user secs. 0.05 sys. secs 0.07 total secs.

Lambda K H  
 0.313 0.136 0.357

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62  
 Gap Penalties: Existence: 11, Extension: 1  
 Number of Hits to DB: 119  
 Number of Sequences: 0  
 Number of extensions: 13

<http://www.ncbi.nlm.nih.gov/blast/bl2seq/wblast2.cgi?>

7/29/2002


Number of successful extensions: 1  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 1  
length of query: 97  
length of database: 327,972,341  
effective HSP length: 73  
effective length of query: 24  
effective length of database: 81,147,807  
effective search space: 1947547368  
effective search space used: 1947547368  
T: 9  
A: 40  
X1: 16 ( 7.2 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 42 (21.8 bits)  
S2: 60 (27.7 bits)



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix  gap open:  gap extension: x\_dropoff:  expect:  wordsize:  Filter ☐ 

Sequence	gi	heat shock 10kD protein 1 (chaperonin 10) [Homo sapiens]	Length 102
1	<u>4504523</u>		

Sequence	gi	GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock	Length 548
2	<u>1790586</u>	protein [Escherichia coli K12]	


No significant similarity was found



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix:  ☒ gap open:  gap extension: x\_dropoff:  expect:  wordsize:  Filter ☐ 

---

Sequence 1 gi\_4504523 heat shock 10kD protein 1 (chaperonin 10) [Homo sapiens] Length 102

Sequence 2 gi\_292160 heat shock protein 70 Length 701

No significant similarity was found





## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix [BLOSUM62](#) gap open: [11](#) gap extension: [1](#)x\_dropoff: [50](#) expect: [10.000](#) wordsize: [3](#) Filter ☐ [Align](#)

---

Sequence 1 gi [4504523](#) heat shock 10kD protein 1 (chaperonin 10) [Homo sapiens] Length 102Sequence 2 gi [32488](#)

Length 732

No significant similarity was found



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix  gap open:  gap extension: x\_dropoff:  expect:  wordsize:  Filter ☐Sequence 1 gi [4504523](#) heat shock 10kD protein 1 (chaperonin 10) [Homo sapiens] Length 102Sequence 2 gi [15010550](#) heat shock protein gp96 precursor [Homo sapiens] Length 782**No significant similarity was found**



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

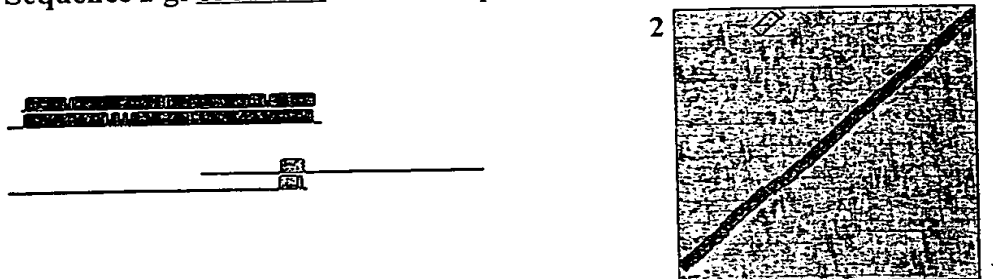
## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix: **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ Align

Sequence 1 gi 32488

Length 732 (1 .. 732)

Sequence 2 gi 15010550 heat shock protein gp96 precursor [Homo sapiens] Length 782 (1 .. 782)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 637 bits (1643), Expect = 0.0  
 Identities = 344/729 (47%), Positives = 479/729 (65%), Gaps = 27/729 (3%)

```

Query:          15  EEVETFAFQAEIAQLMSLIINTFYSNKEIFLRELISNSSDALDKIRYETLTDP SKL
                  E+ E FAFQAE+ ++M LIIN+ Y NKEIFLRELISN+SDALDKIR +LTD + L
Sbjct:          50  EKSEKFAFQAEVNRPMKLIINSLYKNKEIFLRELISNASDALDKIRLISLTDENAL
heat shock protein gp96 50  *****

Query:          75  ELHINLIPNKQDRTLTIVDTGIGMTKADLINNLGTIAKSGTKAFM---EALQAGA
                  EL + + +K+ L + DTG+GMT+ +L+ NLGTIAKSGT F+ EA + G
Sbjct:          110 ELTVKIKCDKEKNLLHVDTGVGMTREELVKNLGTIAKSGTSEFLNKMTEAQEDGQ
heat shock protein gp96 110 *****

Query:          130 MIGQFGVGFYSAYLVAEKVTVITKHNDDEQYAWESSAGGSFTVVRTDTGPEPMGRG TK
                  +IGQFGVGFYSA+LVA+KV V +KHN+D Q+ WES + + G +GRGT
Sbjct:          170 LIGQFGVGFYSAFLVADKVIIVTSKHNNDTQHIWESDSNEFSVIADPRGNTLGRGTT
heat shock protein gp96 170 *****

Query:          190 LKEDQTEYLEERRIKEIVKKHSQFIGYPITLFVEKERDKEVSDDEAEKEDKEEEK
                  LKE+ ++YLE IK +VKK+SQFI +PI ++ K E E+ +EEE
Sbjct:          230 LKEEASDYLELDTIKNLVKKYSQFINFPIYVWSSKT-----ETVEEPMEEEEA
heat shock protein gp96 230 *****

Query:          250 KESEDKPEIEDVGSDEEEKKDGDKKKKKKIKIKEYIDQEELNKT KPIWTRNPDDIT
                  KE D ++ +EEEE+K K K KK+++ D E +N KPIW R ++
Sbjct:          282 KEESD----DEAAVEEEEEEK---KPKTKKVEKTVDWELMNDIKPIWQRPSKEVE
heat shock protein gp96 282 *****
  
```

Query: 310 GEFYKSLTNDWEDHLAVKHFSVEGQLEFRALLFVPRRAPFDLFEN--RKKKNNIKL  
 FYKS + + +D +A HF+ EG++ F+++LFVP AP LF+ KK + IKL  
 Sbjct: 335 KAFYKSFSKESDDPMAYIHFTAEGEVTFSILFVPTSAPRGLFDEYGSKKSDYIKL  
 heat shock protein gp96 335 \*\*\*\*\*

Query: 368 VFIMDNCEELIPEYLNFIIRGVVDSDELPLNISREMLQQSKILKVIKKNLVKKCLEL  
 VFI D+ +++P+YLNFF++GVVDS+DLPLN+SRE LQQ K+LKVIRK LV+K L++  
 Sbjct: 395 VFIPDDFHDMMPKYLNFKGVVDSDDLPLNVSRETLLQHKLLKVIKKNLVKRLTLDL  
 heat shock protein gp96 395 \*\*\*\*\*

Query: 428 AEDKENYKKFYEQFSKNIKLGIIHEDSQNRKKLSELLRYYTSASGDEMVSLLKDYCTR  
 A+DK N F+++F NIKLG+ ED NR +L++LLR+ +S ++ SL Y R  
 Sbjct: 455 ADDKYN-DTFWKEFGTNIKLGVIEDHSNRTRLAKLLRFQSSHPTDITSLDQYVER  
 heat shock protein gp96 455 \*\*\*\*\*

Query: 488 QKHIYYITGETKDQVANSASFVERLRKHGLEVIYMIPIDEYCVQQLKEFEGKTLVS  
 Q IY++ G ++ + +S FVERL K G EVIY+ EP+DEYC+Q L EF+GK +  
 Sbjct: 514 QDKIYFMAGSSRKEAESSPFVERLLKKGYEVIYLTPEVDEYCIQALPEFDGKRFQN  
 heat shock protein gp96 514 \*\*\*\*\*

Query: 548 GLELPEDEEEKKKQEKKTKFENLCKIMKD-ILEKKVEKVVVSNRLVTSPCCIVTS  
 G++ E E+ K+ +E + +FE L MKD L+ K+EK VVS RL SPC +V S  
 Sbjct: 574 GVKFDESEKTKESREAVEKEFEPLLNWMKDKALKDKIEKAVVSQRLTESPCALVAS  
 heat shock protein gp96 574 \*\*\*\*\*

Query: 607 TANMERIMKAQAL---RDNSTMGYMAAKKHLEINPDHSIIETLRQKAEADKNDKSV  
 + NMERIMKAQA +D ST Y + KK EINP H +I + ++ + D++DK+V  
 Sbjct: 634 SGNMERIMKAQAYQTGKDISTNYASQKKTFEINPRHPLIRDMRLRIKEDDDKTV  
 heat shock protein gp96 634 \*\*\*\*\*

Query: 664 ILLYETALLSSGFSLEDPOQHANRIYRMIKLGLGIDEDDPTADDTSAAVTEEMPPL  
 ++L+ETA L SG+ L D + + +RI RM++L L ID D ++ E  
 Sbjct: 694 VVLFETATLRSGYLLPDTKAYGDRIERMLRLSLNIDPDAKVEEPEEPEETAEDT  
 heat shock protein gp96 694 \*\*\*\*\*

Query: 724 DTSRMEEVD 732  
 + EE+D  
 Sbjct: 754 EQDEDEEMD 762  
 heat shock protein gp96 754 \*\*\*\*\*

Score = 35.0 bits (79), Expect = 4.6  
 Identities = 20/61 (32%), Positives = 34/61 (54%), Gaps = 2/61 (3%)

Query: 208 KKHSQFIGYPITLFVEKERDKEVSDDEAEKEDKEEEKEKEESEDKPEIEDVGS  
 K + I + L + + D +V ++ EE E+ E+ ++ ++ ED E DVG+  
 Sbjct: 712 KAYGDRIERMLRLSLNIDPDAKVEEPEEPEETAEDTTEDTEQDED--EEMDVGT  
 heat shock protein gp96 712 \*\*\*\*\*

Query: 268 E 268  
 E  
 Sbjct: 770 E 770  
 heat shock protein gp96 770 \*

CPU time: 0.27 user secs. 0.09 sys. secs 0.36 total secs.

Lambda K H  
 0.312 0.132 0.361

Gapped  
Lambda      K      H  
0.267      0.0410      0.140

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Hits to DB: 12,881  
Number of Sequences: 0  
Number of extensions: 826  
Number of successful extensions: 62  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 1  
Number of HSP's successfully gapped in prelim test: 0  
Number of HSP's that attempted gapping in prelim test: 0  
Number of HSP's gapped (non-prelim): 14  
length of query: 732  
length of database: 327,972,341  
effective HSP length: 131  
effective length of query: 601  
effective length of database: 269,277,922  
effective search space: 161836031122  
effective search space used: 161836031122  
T: 9  
A: 40  
X1: 16 ( 7.2 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 42 (21.8 bits)  
S2: 77 (34.3 bits)

**Blast 2 Sequences results**

PubMed



Entrez

BLAST

OMIM

Taxonomy

Structure

**BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]**Matrix **BLOSUM62**  gap open: **11** gap extension: **1**x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ Sequence  
1 **gi 32488****Length 732**Sequence gi GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock  
2 **1790586** protein [Escherichia coli K12]**Length 548****No significant similarity was found**



## Blast 2 Sequences results

PubMed

Entrez



BLAST

OMIM

Taxonomy

Structure

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix BLOSUM62  gap open: 11 gap extension: 1x\_dropoff: 50 expect: 10.000 wordsize: 3 Filter ☐ 

Sequence 1 gi\_32488

Length 732

Sequence 2 gi\_306890 chaperonin (HSP60) Length 573


No significant similarity was found



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix [BLOSUM62](#) gap open: [11](#) gap extension: [1](#)x\_dropoff: [50](#) expect: [10.000](#) wordsize: [3](#) Filter ☐ Sequence 1 gi [32488](#) Length 732Sequence 2 gi [292160](#) heat shock protein 70 Length 701

No significant similarity was found





## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix:  gap open:  gap extension: x\_dropoff:  expect:  wordsize:  Filter ☐ 

---

Sequence 1 gi [4504523](#) heat shock 10kD protein 1 (chaperonin 10) [Homo sapiens] Length 102Sequence 2 gi [306890](#) chaperonin (HSP60)

Length 573

No significant similarity was found



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix:  gap open:  gap extension: x\_dropoff:  expect:  wordsize:  Filter ☐

Sequence  
1 gi\_306890 chaperonin (HSP60)

**Length 573**

Sequence gi GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP,  
2 1790585 suppressing its ATPase activity [Escherichia coli K12]

**Length 97**

No significant similarity was found



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ **Sequence 1** gi 306890 chaperonin (HSP60) **Length** 573**Sequence 2** gi 292160 heat shock protein 70 **Length** 701**No significant similarity was found**



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix [BLOSUM62](#) gap open:  gap extension: x\_dropoff:  expect:  wordsize:  Filter ☐

Sequence 1 gi\_306890 chaperonin (HSP60)

Length 573

Sequence 2 gi\_15010550 heat shock protein gp96 precursor [Homo sapiens] Length 782

No significant similarity was found



## Blast 2 Sequences results

[PubMed](#)[Entrez](#)[BLAST](#)[OMIM](#)[Taxonomy](#)[Structure](#)

### BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix:  gap open:  gap extension: x\_dropoff:  expect:  wordsize:  Filter ☐

Sequence  
1 gi 292160 heat shock protein 70

Length 701

Sequence gi GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP,  
2 1790585 suppressing its ATPase activity [Escherichia coli K12]

Length 97

No significant similarity was found



# Blast 2 Sequences results

PubMed

Entrez

BLAST

OMIM

Taxonomy

Structure

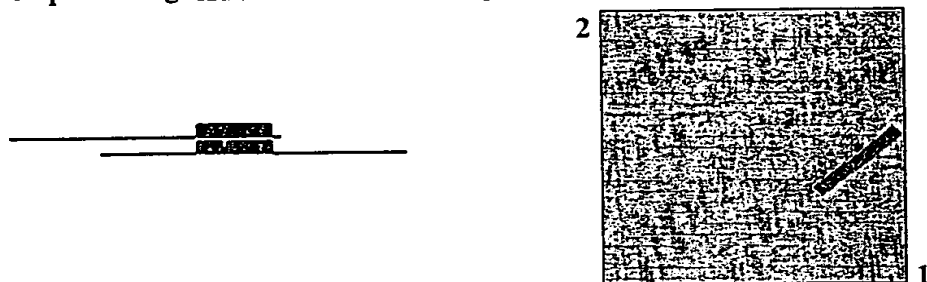
## BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.3 [Apr-24-2002]

Matrix **BLOSUM62** gap open: **11** gap extension: **1**  
 x\_dropoff: **50** expect: **10.000** wordsize: **3** Filter ☐ Align

Sequence 1 gi **292160** heat shock protein 70

Length 701 (1 .. 701)

Sequence 2 gi **15010550** heat shock protein gp96 precursor [Homo sapiens] Length 782 (1 .. 782)



NOTE: The statistics (bitscore and expect value) is calculated based on the size of nr database

Score = 39.3 bits (90), Expect = 0.23

Identities = 44/180 (24%), Positives = 75/180 (41%), Gaps = 7/180 (3%)

```

Query:          502 KSEENEPMETDQNAKEEEKMQVDQEEPHVEEQQQQTPAENKAESEEMETSQAGSK
                  K+E  EEPME ++ AK EEK + D E    EE++++ P  K E    +
Sbjct:          264 KTETVEEPMEEEEAAK-EEKEESDDEAAVEEEEEEEKPKTKKVEKTVWDWELMNDI
heat shock protein gp96 264 *****
Query:          562 DQPPQCQEGKSEDQYCGPANRESAIWQIDREMLNLYIENEGKMIMQDKLEKERNDA
                  +P +  E  ED+Y  A  +S  + D M ++  EG++  + L  +
Sbjct:          323 QRPSKEVE---EDEY--KAFYKSFSKESDDPMAYIHFTAEGEVTFKSILFVPTSAP
heat shock protein gp96 323 *****
Query:          622 EEYVYEMRDKLSGEYEKVFSEDDRNSFTLKLEDTENWLYEDGEDQPKQVYVDKLAE
                  +EY +  D +  +  DD +  K +  +  D +D P V + L +
Sbjct:          378 DEYGSKKSDYIKLYVRRVFI PDDFHDMPKYLNFVKGVV-DSDDLPLNVSRETQQ
heat shock protein gp96 378 *****

```

CPU time: 0.23 user secs. 0.04 sys. secs 0.27 total secs.

Lambda K H  
 0.314 0.131 0.369

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62  
Gap Penalties: Existence: 11, Extension: 1  
Number of Hits to DB: 9115  
Number of Sequences: 0  
Number of extensions: 564  
Number of successful extensions: 9  
Number of sequences better than 10.0: 1  
Number of HSP's better than 10.0 without gapping: 0  
Number of HSP's successfully gapped in prelim test: 1  
Number of HSP's that attempted gapping in prelim test: 2  
Number of HSP's gapped (non-prelim): 6  
length of query: 701  
length of database: 327,972,341  
effective HSP length: 131  
effective length of query: 570  
effective length of database: 266,682,288  
effective search space: 152008904160  
effective search space used: 152008904160  
T: 9  
A: 40  
X1: 16 ( 7.2 bits)  
X2: 129 (49.7 bits)  
X3: 129 (49.7 bits)  
S1: 42 (21.9 bits)  
S2: 76 (33.9 bits)